

5000

43

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/522,827
Source: PU/10
Date Processed by STIC: 2/15/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE).
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/24/05

Raw Sequence Listing Error Summary

ERROR DETECTED

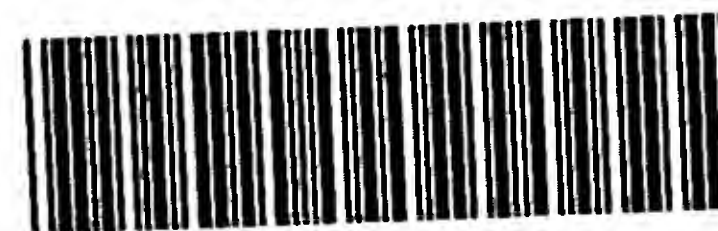
SUGGESTED CORRECTION

SERIAL NUMBER: 10/522,827

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/522,827

DATE: 02/11/2005
TIME: 16:12:58

Input Set : A:\PTO.YF.txt
Output Set: N:\CRF4\02112005\J522827.raw

5 <110> APPLICANT: Lek Pharmaceuticals d. d.
W--> 6 <120> TITLE OF INVENTION: Synthetic gene coding for human granulocyte-colony
W--> 7 stimulating factor for the expression in E. coli
C--> 8 <140> CURRENT APPLICATION NUMBER: US/10/522,827
C--> 8 <141> CURRENT FILING DATE: 2005-01-31
W--> 0 <130> FILE REFERENCE:
W--> 8 <160> NUMBER OF SEQ ID: 2

see p. 2

ERRORED SEQUENCES

E--> 11 <210> SEQ ID NO: SEQ ID NO: 1
12 <211> LENGTH: 525 base pairs
13 <212> TYPE: DNA
14 <213> ORGANISM: synthetic sequence

W--> 15 <220> FEATURE: gene

W--> 16 <400> SEQUENCE: SEQ ID NO: 1

E--> 18 atgacaccac tgggtccagc ttcttctctg ccgcaaagct ttctgttgaa atgttttagaa
E--> 19 caagttcgta aaattcaagg tgatggtgca gctttacaag aaaaactgtg tgcaacttat
E--> 20 aaactgtgtc atccagaaga actggttctg ttaggtcatt ctctgggtat tccgtgggct
E--> 21 cctctgagct cctgtccgag ccaggcgtg cagctggcag gctgcctgag ccaactgcat
E--> 22 agcggctctgt ttctgtatca gggctctgctg caggcgtgg aaggcatttc cccggaactg
E--> 23 gggccacact tggacacact gcagctggac gtcgccgact ttgccaccac catctggcag
E--> 24 cagatggaag aactgggaat ggcccctgcc ctgcagccca cccagggtgc catgccggcc
E--> 25 ttcgcctctg ctttccagcg ccgtgcaggt ggggtcctgg ttgctagcca tctgcaatct
E--> 26 tttctggaag ttagctatcg tgttctgcgt catctggctc agccg

E--> 28 <210> SEQ ID NO: SEQ ID NO: 2
29 <211> LENGTH: 528 base pairs
30 <212> TYPE: DNA
31 <213> ORGANISM: synthetic sequence

W--> 32 <220> FEATURE: gene

W--> 33 <400> SEQUENCE: SEQ ID NO: 2

E--> 34 atgacaccac tgggtccagc ttcttctctg ccgcaaagct ttctgttgaa atgttttagaa
E--> 35 caagttcgta aaattcaagg tgatggtgca gctttacaag aaaaactgtg tgcaacttat
E--> 36 aaactgtgtc atccagaaga actggttctg ttaggtcatt ctctgggtat tccgtgggct
E--> 37 cctctgagct cctgtccgag ccaggcgtg cagctggcag gctgcctgag ccaactgcat
E--> 38 agcggctctgt ttctgtatca gggctctgctg caggcgtgg aaggcatttc cccggaactg
E--> 39 gggccacact tggacacact gcagctggac gtcgccgact ttgccaccac catctggcag
E--> 40 cagatggaag aactgggaat ggcccctgcc ctgcagccca cccagggtgc catgccggcc
E--> 41 ttcgcctctg ctttccagcg ccgtgcaggt ggggtcctgg ttgctagcca tctgcaatct
E--> 42 tttctggaag ttagctatcg tgttctgcgt catctggctc agccgtga

**Does Not Comply
Corrected Diskette Needed**

see item 4 on summary sheet

10/5/82

2

SEQUENCE LISTING

<110> Lek Pharmaceuticals d. d.
<120> Synthetic gene coding for human granulocyte-colony
stimulating factor for the expression in E. coli
<160> 2

add these mandatory
numeric
identifiers
and
responses

delete - do NOT insert alphabetical
headings

<210> ~~SEQ ID NO: 1~~
<211> 525 base pairs
<212> DNA

<213> synthetic sequence

<220> ~~gene~~ delete - do NOT insert any response
to <220>

<400> ~~SEQ ID NO: 1~~
delete

atgacaccac tgggtccagc ttcttctctg ccgcaaagct ttctgttgaa atgttttagaa
caagtctgta aaattcaagg tgatggtgca gctttacaag aaaaactgtg tgcaacttat
aaactgtgtc atccagaaga actggttctg ttaggtcatt ctctgggtat tccgtgggct
cctctgagct cctgtccgag ccaggcgtg cagctggcag gctgcctgag ccaactgcat
agcggctctg ttctgtatca gggctctgctg caggcgtggt aaggcatttc cccggaactg
gggcccacct tggacacact gcagctggac gtcgccgact ttgccaccac catctggcag
cagatggaag aactgggaat ggcccctgcc ctgcagccca cccagggtgc catgccggcc
ttcgccctctg ctttccagcg ccgtgcaggt ggggtcctgg ttgctagcca tctgcaatct
tttctggaag ttagctatcg tgttctgcgt catctggctc agccg

60
120

Per 1.822
of sequence
rules,
insert
cumulative
base totals
at right
margin of
each
line

<210> ~~SEQ ID NO: 2~~
<211> 528 base pairs
<212> DNA

<213> synthetic sequence

<220> ~~gene~~ FYI: "gene" is not a sufficient explanation
for <213> Artificial Sequence

<400> ~~SEQ ID NO: 2~~

atgacaccac tgggtccagc ttcttctctg ccgcaaagct ttctgttgaa atgttttagaa
caagtctgta aaattcaagg tgatggtgca gctttacaag aaaaactgtg tgcaacttat
aaactgtgtc atccagaaga actggttctg ttaggtcatt ctctgggtat tccgtgggct
cctctgagct cctgtccgag ccaggcgtg cagctggcag gctgcctgag ccaactgcat
agcggctctg ttctgtatca gggctctgctg caggcgtggt aaggcatttc cccggaactg
gggcccacct tggacacact gcagctggac gtcgccgact ttgccaccac catctggcag
cagatggaag aactgggaat ggcccctgcc ctgcagccca cccagggtgc catgccggcc
ttcgccctctg ctttccagcg ccgtgcaggt ggggtcctgg ttgctagcca tctgcaatct
tttctggaag ttagctatcg tgttctgcgt catctggctc agccgtga

same
error

1) Consult Sequence Rules
for VALID format

2) Consult sample Sequence Listing, attached

<110> Smith, John; Smithgene Inc.
 <120> Example of a Sequence Listing
 <130> 01-00001
 <140> PCT/EP98/00001
 <141> 1998-12-31
 <150> US 08/999,999
 <151> 1997-10-15
 <160> 4
 <170> PatentIn version 2.0
 <210> 1
 <211> 389
 <212> DNA
 <213> Paramecium sp.
 <220>
 <221> CDS
 <222> (279)...(389)
 <300>
 <301> Doe, Richard
 <302> Isolation and Characterization of a Gene Encoding a
 Protease from Paramecium sp.
 <303> Journal of Genes
 <304> 1
 <305> 4
 <306> 1-7
 <307> 1988-06-31
 <308> 123456
 <309> 1988-06-31
 <400> 1
 agctgtagtc attcctgtgt cctcttctct ctgggcttct caccctgcta atcagatctc 60
 agggagagtg tcttgaccct cctctgcctt tgcagcttca caggcaggca ggcaggcagc 120
 tgatgtggca attgctggca gtgccacagg cttttcagcc aggettaggg tgggttccgc 180
 cgcggcgcgg cggccccctc cgcgctctc tgcgcctct ctctcgctct cctctcgctc 240

Consult this

ggacctgatt	aggtgagcag	gaggaggggg	cagtttagc	atg Met 1	gtt Val	tca Ser	atg Met	ttc Phe 5	agc Ser	296
------------	------------	------------	-----------	-----------------	------------	------------	------------	-----------------	------------	-----

ttg Leu	tct Ser	ttc Phe	aaa Lys 10	tgg Trp	cct Pro	gga Gly	ttt Phe	tgt Cys 15	ttg Leu	ttt Phe	gtt Val	tgt Cys	ttg Leu 20	ttc Phe	caa Gln	344
------------	------------	------------	------------------	------------	------------	------------	------------	------------------	------------	------------	------------	------------	------------------	------------	------------	-----

tgt Cys	ccc Pro	aaa Lys 25	gtc Val	ctc Leu	ccc Pro	tgt Cys	cac His 30	tca Ser	tca Ser	ctg Leu	cag Gln	ccg Pro 35	aat Asn	ctt Leu	389
------------	------------	------------------	------------	------------	------------	------------	------------------	------------	------------	------------	------------	------------------	------------	------------	-----

<210> 2
 <211> 37
 <212> PRT
 <213> Paramecium sp.

<400> 2 Met 1	Val	Ser	Met	Phe 5	Ser	Leu	Ser	Phe	Lys 10	Trp	Pro	Gly	Phe	Cys 15	Leu
---------------------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----

Phe	Val	Cys	Leu 20	Phe	Gln	Cys	Pro	Lys 25	Val	Leu	Pro	Cys	His 30	Ser	Ser
-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----	-----	-----	-----------	-----	-----

Leu	Gln	Pro 35	Asn	Leu
-----	-----	-----------	-----	-----

<210> 3
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Designed peptide based on size and polarity to act as a linker between the alpha and beta chains of Protein XYZ.

<400> 3 Met 1	Val	Asn	Leu	Glu 5	Pro	Met	His	Thr	Glu 10	Ile
---------------------	-----	-----	-----	----------	-----	-----	-----	-----	-----------	-----

<210> 4
 <400> 4
 000

identifiers and their accompanying information as shown in the following table. The numeric identifier shall be used only in the "Sequence Listing." The order and presentation of the items of information in the "Sequence Listing" shall conform to the arrangement given below. Each item of information shall begin on a new line and shall begin with the numeric identifier enclosed in angle brackets as shown. The submission of those items of information designated with an "M" is mandatory. The submission of those items of information designated with an "O" is optional. Numeric identifiers <110> through <170> shall only be set forth at the beginning of the "Sequence Listing." The following table illustrates the numeric identifiers.

Numeric Identifier	Definition	Comments and Format	Mandatory (M) or Optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable include priority documents under 35 USC 119 and 120
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M
<170>	Software	Name of software used to create the Sequence Listing	O
<210>	SEQ ID NO:#:	Response shall be an integer representing the SEQ ID NO shown	M
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues	M

<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M
<213>	Organism	Scientific name, i.e. Genus/species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<221>	Name/Key	Provide appropriate identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/amino acids	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified

		in feature	base was used in a sequence
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	0
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials	0
<302>	Title		0
<303>	Journal		0
<304>	Volume		0
<305>	Issue		0
<306>	Pages		0
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy	0
<308>	Database Accession Number	Accession number assigned by database including database name	0
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy	0
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999	0

<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd	O
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd	O
<313>	Relevant Residues	FROM (position) TO (position)	O
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence	M

5. Section 1.824 is revised to read as follows:

1.824 Form and format for nucleotide and/or amino acid sequence submissions in computer readable form.

(a) The computer readable form required by 1.821(e) shall meet the following specifications:

(1) The computer readable form shall contain a single "Sequence Listing" as either a diskette, series of diskettes, or other permissible media outlined in paragraph (c) of this section.

(2) The "Sequence Listing" in paragraph (a) (1) of this section shall be submitted in American Standard Code for Information Interchange (ASCII) text. No other formats shall be allowed.

(3) The computer readable form may be created by any means, such as word processors, nucleotide/amino acid sequence editors or other custom computer programs; however, it shall conform to all specifications detailed in this section.

(4) File compression is acceptable when using diskette media, so long as the compressed file is in a self-extracting format that will decompress on one of the systems described in paragraph (b) of this section.

(5) Page numbering shall not appear within the computer readable form version of the "Sequence Listing" file.

(6) All computer readable forms shall have a label permanently affixed thereto on which has been hand-printed or typed: the name of the applicant, the title of the invention, the date on which the data were recorded on the computer readable form, the operating system used, a reference number, and an application serial number and filing date, if known.

(b) Computer readable form submissions must meet these format requirements:

(1) Computer: IBM PC/XT/AT, or compatibles, or Apple Macintosh;

(2) Operating System: MS-DOS, Unix or Macintosh;